

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 8, 2003, 14:26:12 ; Search time 27 Seconds

(without alignments)  
837.207 Million cell updates/sec

Title: US-09-001-737-8

Perfect score: 545

Sequence: 1 MAKEIRFSADARAAWRCVGD.....TPAPAMPAGMDPGMGMGCG 545

Scoring table: OLIGO

Searched: 112892 segs, 41476328 residues

Word size : 8

Total number of hits satisfying chosen parameters: 222

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Listing first 1000 summaries

Database : SWISSProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|----|-------------|
| 1          | 538   | 98.7  | 542    | 1  | CH60_STRPY  |
| 2          | 56    | 10.3  | 542    | 1  | CH60_LACIA  |
| 3          | 32    | 5.9   | 540    | 1  | CH60_LACIE  |
| 4          | 31    | 5.7   | 542    | 1  | CH60_LISMO  |
| 5          | 27    | 5.0   | 544    | 1  | CH60_AGRPS  |
| 6          | 27    | 5.0   | 545    | 1  | CH61_RHIME  |
| 7          | 27    | 5.0   | 545    | 1  | CH64_RHIME  |
| 8          | 27    | 5.0   | 547    | 1  | CH60_BORPE  |
| 9          | 26    | 4.8   | 538    | 1  | CH60_STRAU  |
| 10         | 26    | 4.8   | 542    | 1  | CH60_LISIN  |
| 11         | 26    | 4.8   | 542    | 1  | CH65_RHIME  |
| 12         | 25    | 4.6   | 539    | 1  | CH60_BACST  |
| 13         | 25    | 4.6   | 540    | 1  | CH60_CLOTM  |
| 14         | 25    | 4.6   | 544    | 1  | CH60_BACHD  |
| 15         | 25    | 4.6   | 546    | 1  | CH60_BURCE  |
| 16         | 25    | 4.6   | 546    | 1  | CH60_BURRS  |
| 17         | 25    | 4.6   | 546    | 1  | CH60_BURH   |
| 18         | 25    | 4.6   | 546    | 1  | CH60_BURVI  |
| 19         | 24    | 4.4   | 538    | 1  | CH60_BACB3  |
| 20         | 24    | 4.4   | 539    | 1  | CH61_BRAJA  |
| 21         | 24    | 4.4   | 543    | 1  | CH60_BACSU  |
| 22         | 24    | 4.4   | 543    | 1  | CH60_CLOLM  |
| 23         | 24    | 4.4   | 543    | 1  | CH60_CHLTR  |
| 24         | 24    | 4.4   | 544    | 1  | CH60_CHLDP  |
| 25         | 24    | 4.4   | 544    | 1  | CH60_CHLDS  |
| 26         | 24    | 4.4   | 545    | 1  | CH60_CAME   |
| 27         | 24    | 4.4   | 545    | 1  | CH60_PORGI  |
| 28         | 24    | 4.4   | 546    | 1  | CH60_BROUB  |
| 29         | 23    | 4.2   | 543    | 1  | CH60_CLOAB  |
| 30         | 23    | 4.2   | 545    | 1  | CH60_PSEBU  |
| 31         | 23    | 4.2   | 546    | 1  | CH60_CHRVT  |
| 32         | 23    | 4.2   | 547    | 1  | CH60_CAIOR  |
| 33         | 23    | 4.2   | 547    | 1  | CH60_PSEPE  |

|     |    |     |     |   |            |                     |
|-----|----|-----|-----|---|------------|---------------------|
| 34  | 22 | 4.0 | 529 | 1 | CH60_GUTH  | 078419 guillardia   |
| 35  | 22 | 4.0 | 547 | 1 | CH60_BARE  | 033963 bartonella   |
| 36  | 22 | 4.0 | 547 | 1 | CH60_BARO  | 033964 bartonella   |
| 37  | 22 | 4.0 | 548 | 1 | CH60_ZYMO  | P48320 zymomonas m  |
| 38  | 22 | 4.0 | 548 | 1 | CH60_PYRS  | P46324 pyrenomonas  |
| 39  | 21 | 3.9 | 540 | 1 | CH61_SYNR3 | 005972 synecocyst   |
| 40  | 21 | 3.9 | 541 | 1 | CH60_CTRPA | 037757 cyanophora   |
| 41  | 21 | 3.9 | 544 | 1 | CH61_SYNVU | 050383 synecococc   |
| 42  | 21 | 3.9 | 552 | 1 | CH60_COXBU | P19421 coxiella bu  |
| 43  | 21 | 3.9 | 552 | 1 | CH60_PSEST | 033500 pseudomonas  |
| 44  | 20 | 3.7 | 539 | 1 | CH62_MYCPA | P06806 mycobacteri  |
| 45  | 20 | 3.7 | 540 | 1 | CH60_MYCPA | P42384 mycobacteri  |
| 46  | 20 | 3.7 | 540 | 1 | CH62_MYCLE | P09939 mycobacteri  |
| 47  | 20 | 3.7 | 543 | 1 | CH60_BABA  | P35635 bartonella   |
| 48  | 20 | 3.7 | 546 | 1 | CH60_RHIV  | P34839 rhizodulum 1 |
| 49  | 19 | 3.5 | 300 | 1 | CH60_STNP6 | P12834 synecococc   |
| 50  | 19 | 3.5 | 540 | 1 | CH60_THERB | 060024 thermobacter |
| 51  | 19 | 3.5 | 542 | 1 | CH62_RHIME | P35470 rhizodulum m |
| 52  | 19 | 3.5 | 544 | 1 | CH60_SYN7  | P22879 synecococc   |
| 53  | 19 | 3.5 | 545 | 1 | CH63_BRAJA | P35862 bradyrhizob  |
| 54  | 19 | 3.5 | 546 | 1 | CH60_LEPIN | P35468 leptospira   |
| 55  | 19 | 3.5 | 549 | 1 | CH62_BRAJA | P35861 bradyrhizob  |
| 56  | 18 | 3.3 | 538 | 1 | CH60_STAP  | P48318 staphylococ  |
| 57  | 18 | 3.3 | 542 | 1 | CH60_THERH | P45746 thermus the  |
| 58  | 18 | 3.3 | 544 | 1 | CH60_FRATU | P94798 francisella  |
| 59  | 17 | 3.1 | 539 | 1 | CH61_MYCTU | 059573 mycobacteri  |
| 60  | 17 | 3.1 | 544 | 1 | CH63_RHIME | 093050 rhizodulum m |
| 61  | 17 | 3.1 | 476 | 1 | CH62_STRL1 | 033658 streptomyc   |
| 62  | 16 | 2.9 | 539 | 1 | CH60_CLOPE | P26821 clostridium  |
| 63  | 16 | 2.9 | 539 | 1 | CH61_STRAL | 000767 streptomyc   |
| 64  | 16 | 2.9 | 539 | 1 | CH62_STRAL | 000768 streptomyc   |
| 65  | 16 | 2.9 | 540 | 1 | CH61_STRCO | P40171 streptomyc   |
| 66  | 16 | 2.9 | 540 | 1 | CH61_STRLI | 033659 streptomyc   |
| 67  | 16 | 2.9 | 543 | 1 | CH60_MYCE  | P33659 streptomyc   |
| 68  | 16 | 2.9 | 543 | 1 | CH60_MYCPA | P78032 mycoplasma   |
| 69  | 16 | 2.9 | 544 | 1 | CH60_NEIFL | P48215 neisseria f  |
| 70  | 16 | 2.9 | 544 | 1 | CH60_NEIGO | P29842 neisseria g  |
| 71  | 16 | 2.9 | 544 | 1 | CH60_NEIMA | P57006 neisseria m  |
| 72  | 16 | 2.9 | 548 | 1 | CH60_NEIMA | P42385 neisseria m  |
| 73  | 16 | 2.9 | 548 | 1 | CH60_EHRI1 | P48214 entrichia r  |
| 74  | 16 | 2.9 | 548 | 1 | CH60_EHRIE | 032606 entrichia r  |
| 75  | 15 | 2.8 | 534 | 1 | CH60_GALSU | P28295 galdieria s  |
| 76  | 15 | 2.8 | 534 | 1 | CH60_ENTNG | 066300 enterobacte  |
| 77  | 15 | 2.8 | 538 | 1 | CH60_ENTNG | 066196 enterobacte  |
| 78  | 15 | 2.8 | 539 | 1 | CH60_ENTAS | 066192 enterobacte  |
| 79  | 15 | 2.8 | 539 | 1 | CH60_ENTIT | 066192 enterobacte  |
| 80  | 15 | 2.8 | 539 | 1 | CH60_SERRU | 066202 serratia ru  |
| 81  | 15 | 2.8 | 540 | 1 | CH60_ENTAE | 066198 enterobacte  |
| 82  | 15 | 2.8 | 540 | 1 | CH60_ENTGE | 066194 enterobacte  |
| 83  | 15 | 2.8 | 540 | 1 | CH60_ERMAP | 066222 erwilia aph  |
| 84  | 15 | 2.8 | 540 | 1 | CH60_ERMAP | 066220 erwilia aph  |
| 85  | 15 | 2.8 | 540 | 1 | CH60_KLEON | 066214 klebsiella   |
| 86  | 15 | 2.8 | 540 | 1 | CH60_KLEBX | 066210 klebsiella   |
| 87  | 15 | 2.8 | 540 | 1 | CH60_KLEPL | 066212 klebsiella   |
| 88  | 15 | 2.8 | 540 | 1 | CH60_SERTI | 066204 serratia fi  |
| 89  | 15 | 2.8 | 541 | 1 | CH60_ERWHE | 066216 erwilia her  |
| 90  | 15 | 2.8 | 541 | 1 | CH60_PANAN | 066218 pantoea ana  |
| 91  | 15 | 2.8 | 544 | 1 | CH60_AERNA | 066309 aeromonas s  |
| 92  | 15 | 2.8 | 545 | 1 | CH60_BORBU | P27575 borrelia bu  |
| 93  | 15 | 2.8 | 545 | 1 | CH60_PANDE | 094462 paracoccus   |
| 94  | 15 | 2.8 | 545 | 1 | CH60_RHOCA | P95678 rhodobacter  |
| 95  | 15 | 2.8 | 545 | 1 | CH60_SODGL | 096nr8 sodalis glo  |
| 96  | 15 | 2.8 | 546 | 1 | CH60_ACTAC | P46398 actinobacil  |
| 97  | 15 | 2.8 | 546 | 1 | CH60_ACTAC | P46398 actinobacil  |
| 98  | 15 | 2.8 | 546 | 1 | CH60_LEONI | P26194 legionella   |
| 99  | 15 | 2.8 | 546 | 1 | CH60_WIGGL | 096nr9 wigglieswort |
| 100 | 15 | 2.8 | 546 | 1 | CH60_RHOSH | P20110 rhodobacter  |
| 101 | 15 | 2.8 | 547 | 1 | CH60_ALTHA | 096xau7 alteromonas |
| 102 | 15 | 2.8 | 547 | 1 | CH60_ECOLI | P06139 escherichia  |
| 103 | 15 | 2.8 | 547 | 1 | CH60_HARDU | P31294 hemophilus   |
| 104 | 15 | 2.8 | 547 | 1 | CH60_KLEPN | 066026 klebsiella   |
| 105 | 15 | 2.8 | 547 | 1 | CH60_LEGPN | P26878 legionella   |
| 106 | 15 | 2.8 | 547 | 1 | CH60_PASMU | 059687 pasteurella  |

|     |    |     |     |   |            |                     |     |    |     |      |   |            |                    |
|-----|----|-----|-----|---|------------|---------------------|-----|----|-----|------|---|------------|--------------------|
| 107 | 15 | 2.8 | 547 | 1 | CH60_SALTY | P48217 salmonella   | 180 | 11 | 2.0 | 530  | 1 | CH60_CYACA | 09111 cyanidium c  |
| 108 | 15 | 2.8 | 548 | 1 | CH60_BUCAI | P25750 buchiera ap  | 181 | 11 | 2.0 | 554  | 1 | CH60_HOLOB | P34820 holospora o |
| 109 | 15 | 2.8 | 548 | 1 | CH60_BUCMP | O51832 buchiera ap  | 182 | 11 | 2.0 | 562  | 1 | CH60_TYRBB | O37663 trypanosoma |
| 110 | 15 | 2.8 | 548 | 1 | CH60_HAEIN | P43733 haemophilus  | 183 | 11 | 2.0 | 562  | 1 | CH60_TYRBR | O95046 trypanosoma |
| 111 | 15 | 2.8 | 550 | 1 | CH60_XARMA | P95800 xanthomonas  | 184 | 11 | 2.0 | 562  | 1 | CH60_CAEEL | P50140 caenorhabdi |
| 112 | 15 | 2.8 | 551 | 1 | CH60_YEREN | P48215 yerstinia en | 185 | 11 | 2.0 | 568  | 1 | CH60_EUGGR | O39727 euglena gra |
| 113 | 15 | 2.8 | 551 | 1 | CH60_AMOPS | P28004 amoeba prot  | 186 | 11 | 2.0 | 583  | 1 | RUB2_BRANA | P34794 brassica na |
| 114 | 15 | 2.8 | 551 | 1 | CH60_BUCAP | O59177 buchiera ap  | 187 | 11 | 2.0 | 586  | 1 | RUBA_ARATH | P21288 arabidopsis |
| 115 | 15 | 2.8 | 566 | 1 | CH60_CANAL | O74261 candida alb  | 188 | 11 | 2.0 | 589  | 1 | CH60_LEITA | O44566 leishmania  |
| 116 | 15 | 2.8 | 566 | 1 | CH60_HELYI | P25420 heliothis v  | 189 | 11 | 2.0 | 648  | 1 | CH60_DROME | O49566 drosophila  |
| 117 | 15 | 2.8 | 573 | 1 | CH60_CRIGR | P18687 cricetus     | 190 | 10 | 1.8 | 495  | 1 | RUBA_WHEAT | O3965 drosophila   |
| 118 | 15 | 2.8 | 573 | 1 | CH60_DROME | O02649 drosophila   | 191 | 10 | 1.8 | 543  | 1 | RUBA_RICCO | P08823 ricinus com |
| 119 | 15 | 2.8 | 573 | 1 | CH60_HUMAN | P19226 mus musculu  | 192 | 10 | 1.8 | 575  | 1 | CH61_CUCMA | O05045 cucurbita m |
| 120 | 15 | 2.8 | 573 | 1 | CH60_MOUSE | O97055 drosophila   | 193 | 10 | 1.8 | 575  | 1 | CH62_CUCMA | O05046 cucurbita m |
| 121 | 15 | 2.8 | 573 | 1 | CH6C_DROME | O97055 drosophila   | 194 | 10 | 1.8 | 576  | 1 | CH62_MAIZE | O43298 zea mays (m |
| 122 | 15 | 2.8 | 408 | 1 | CH60_BACFO | P81284 bacteroides  | 195 | 10 | 1.8 | 577  | 1 | CH60_ARATH | P29197 arabidopsis |
| 123 | 14 | 2.6 | 408 | 1 | CH60_RICRI | O34198 rickettsia   | 196 | 10 | 1.8 | 577  | 1 | CH60_MAIZE | P29197 arabidopsis |
| 124 | 14 | 2.6 | 426 | 1 | CH60_RICRY | O85754 rickettsia   | 197 | 10 | 1.8 | 580  | 1 | RUBA_CHLRE | O42654 chlamydomon |
| 125 | 14 | 2.6 | 435 | 1 | RUBB_CHLRE | O42653 chlamydomon  | 198 | 10 | 1.8 | 587  | 1 | RUBA_BRANA | O42654 chlamydomon |
| 126 | 14 | 2.6 | 528 | 1 | CH60_ODOSI | P9464 odontella s   | 199 | 10 | 1.8 | 587  | 1 | RUBA_BRANA | O42654 chlamydomon |
| 127 | 14 | 2.6 | 537 | 1 | CH60_PORPU | P51349 porphyra pu  | 200 | 9  | 1.7 | 587  | 1 | RUBA_PEA   | O42654 chlamydomon |
| 128 | 14 | 2.6 | 538 | 1 | CH61_MYLE  | P37578 mycobacteri  | 201 | 8  | 1.5 | 40   | 1 | CH60_LEITA | O42654 chlamydomon |
| 129 | 14 | 2.6 | 540 | 1 | CH60_THEMA | O9WYX6 thermocoga   | 202 | 8  | 1.5 | 35   | 1 | CH60_SOLTU | P05052 solanum tub |
| 130 | 14 | 2.6 | 540 | 1 | CH60_SERMA | O66206 serratia ma  | 203 | 8  | 1.5 | 355  | 1 | YDPe_SCHPO | O14009 schizosacch |
| 131 | 14 | 2.6 | 541 | 1 | CH60_TROWH | O9XJ50 tropheryma   | 204 | 8  | 1.5 | 441  | 1 | YDPe_SCHPO | O14009 schizosacch |
| 132 | 14 | 2.6 | 543 | 1 | CH62_RHOSH | P95647 rhodobacter  | 205 | 8  | 1.5 | 441  | 1 | ZRAR_SALTY | O82333 salmonella  |
| 133 | 14 | 2.6 | 543 | 1 | CH62_STYNU | O57002 synecococc   | 206 | 8  | 1.5 | 542  | 1 | ZRAR_SALTY | O82333 salmonella  |
| 134 | 14 | 2.6 | 546 | 1 | RUB1_BRANA | P21239 brassica na  | 207 | 8  | 1.5 | 543  | 1 | THSA_METH  | O26330 methanobact |
| 135 | 14 | 2.6 | 546 | 1 | CH60_RICPR | O92H04 rickettsia   | 208 | 8  | 1.5 | 545  | 1 | THSA_THERC | O26330 methanobact |
| 136 | 14 | 2.6 | 550 | 1 | CH60_RICPR | O92H04 rickettsia   | 209 | 8  | 1.5 | 545  | 1 | THSB_ARCTU | O28805 archaeoglob |
| 137 | 14 | 2.6 | 551 | 1 | CH62_SYNS3 | P22034 synecocyst   | 210 | 8  | 1.5 | 545  | 1 | THSB_THER8 | O24732 thermococu  |
| 138 | 14 | 2.6 | 572 | 1 | HS60_YEAST | P19882 saccharomyc  | 211 | 8  | 1.5 | 545  | 1 | THSB_THER8 | O24732 thermococu  |
| 139 | 14 | 2.6 | 590 | 1 | HS60_AJECA | P50142 atellomycet  | 212 | 8  | 1.5 | 546  | 1 | THSB_PYRKO | O25300 pyrococcus  |
| 140 | 14 | 2.6 | 592 | 1 | HS60_PABBR | O60008 paracoccidi  | 213 | 8  | 1.5 | 546  | 1 | THSB_PYRKO | O24730 pyrococcus  |
| 141 | 13 | 2.4 | 543 | 1 | CH60_TREPA | P23033 treponema p  | 214 | 8  | 1.5 | 549  | 1 | THSA_THER1 | O24729 pyrococcus  |
| 142 | 13 | 2.4 | 546 | 1 | CH60_HELPT | O32N08 helicobacte  | 215 | 8  | 1.5 | 549  | 1 | THSA_THER8 | O24729 pyrococcus  |
| 143 | 13 | 2.4 | 546 | 1 | CH60_HELPT | P42383 helicobacte  | 216 | 8  | 1.5 | 550  | 1 | THS_PYRAB  | O24729 pyrococcus  |
| 144 | 13 | 2.4 | 588 | 1 | RUBB_BRANA | P1241 brassica na   | 217 | 8  | 1.5 | 556  | 1 | THS_PYRAB  | O24729 pyrococcus  |
| 145 | 13 | 2.4 | 595 | 1 | RUBC_PEA   | P08927 pisum sativ  | 218 | 8  | 1.5 | 557  | 1 | THS2_HALVI | O9V972 pyrococcus  |
| 146 | 13 | 2.4 | 600 | 1 | RUBC_ARATH | P21240 arabidops    | 219 | 8  | 1.5 | 700  | 1 | THS2_HALVI | O9V972 pyrococcus  |
| 147 | 12 | 2.2 | 259 | 1 | RUBC_CHLRE | O42695 chlamydomon  | 220 | 8  | 1.5 | 946  | 1 | AMPN_PLIAG | O30560 halobacteri |
| 148 | 12 | 2.2 | 470 | 1 | CH60_EHRTA | O34194 ehrlchia c   | 221 | 8  | 1.5 | 1286 | 1 | AMPN_PLIAG | O30560 halobacteri |
| 149 | 12 | 2.2 | 470 | 1 | CH60_TRIYA | O59508 trichomonas  | 222 | 8  | 1.5 | 1520 | 1 | ABL_DROME  | P34940 plasmodium  |
| 150 | 12 | 2.2 | 541 | 1 | CH60_ANAPH | O34191 anaplasmia p |     |    |     |      |   |            | P34940 plasmodium  |
| 151 | 12 | 2.2 | 545 | 1 | CH60_AQUAE | O67943 equitex ae   |     |    |     |      |   |            | P34940 plasmodium  |
| 152 | 12 | 2.2 | 550 | 1 | CH60_EURCH | P42382 ehrlchia c   |     |    |     |      |   |            | P34940 plasmodium  |
| 153 | 12 | 2.2 | 551 | 1 | CH60_COMRU | P48213 cowdria rum  |     |    |     |      |   |            | P34940 plasmodium  |
| 154 | 12 | 2.2 | 555 | 1 | CH60_RICTS | P16625 rickettsia   |     |    |     |      |   |            | P34940 plasmodium  |
| 155 | 12 | 2.2 | 582 | 1 | HS60_SCHPO | O09864 schizosacch  |     |    |     |      |   |            | P34940 plasmodium  |
| 156 | 11 | 2.0 | 114 | 1 | CH60_MYCUL | O50826 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 157 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48883 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 158 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 159 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 160 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 161 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 162 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 163 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 164 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 165 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 166 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 167 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 168 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
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| 170 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 171 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 172 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 173 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 174 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 175 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 176 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 177 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 178 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |
| 179 | 11 | 2.0 | 120 | 1 | CH60_MYCAG | O48884 mycobacteri  |     |    |     |      |   |            | P34940 plasmodium  |

## ALIGNMENTS

RESULT 1  
CH60\_STREPY STANDARD; PRT: 542 AA.  
AC P82485; 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).  
GN GROU OR MOPR OR GROEL OR SPY2070.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobactillales; Streptococcaceae;  
CC Streptococcus.  
OX NCBI-TaxID-1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;  
RX MEDLINE-21192684; PubMed-11296296;  
RA Ferretti J.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
RA Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,  
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,  
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes".  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
RN [2]  
RP PARTIAL SEQUENCE, AND MASS SPECTROMETRY.

RC STRAIN-JRS4 / Serotype M6;  
 RA Hogan D.A., Du P., Stevenson T.I., Whittton M., Kilby G.W., Rogers J.,  
 RA Vanbogaert R.A.;  
 RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes  
 proteins".  
 RT Submitted (May-2000) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
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 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
 CC 7 SUBUNITS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
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 CC EMBL: AE006627; AAK34727.1; -  
 DR HSSP: P06139; 1GRU.  
 DR InterPro: IPR001844; Chaprnln\_Cpn60.  
 DR InterPro: IPR002423; Cpn60/TCP-1.  
 DR Pfam: PF00118; Cpn60\_TCP1.1.  
 DR PRINTS: PR00298; CHAPERONIN60.  
 DR PROSITE: PS00296; TCMPLXTCPI.  
 DR PROSITE: PS00296; CHAPERONIN60; 1.  
 DR Chaperone: Heat shock; ATP-binding; Complete proteome.  
 RT INIT\_MET 0  
 RT SEQUENCE 542 AA; 56964 MW; C7B9A139BFD71D4 CRC64;  
 SO  
 Query Match 98.7%; Score 538; DB 1; Length 542;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 INFSADARAAMVRCVMDLADTVKTLGPKGRNVLEKAGSPFLITNDGVTAKETIEDH 64  
 DB 4 IFSADARAAMVRCVMDLADTVKTLGPKGRNVLEKAGSPFLITNDGVTAKETIEDH 63  
 QY 65 FENMGAKVSVASKTNDIAGDGTATVTAQVYHEGKNTAGCANPTGIRGCIETATA 124  
 DB 64 FENMGAKVSVASKTNDIAGDGTATVTAQVYHEGKNTAGCANPTGIRGCIETATA 123  
 QY 123 TAVEALKAIAPVSGKEALIAQVAVSSRSKGYEYISEMERVNDGYITTEESRGHETE 184  
 DB 124 TAVEALKAIAPVSGKEALIAQVAVSSRSKGYEYISEMERVNDGYITTEESRGHETE 183  
 QY 185 LEVVEGMOFDDGYISQYVWYDNKEMVADLENPFILITDKKYSNIODILPLEEVLKTNRP 244  
 DB 184 LEVVEGMOFDDGYISQYVWYDNKEMVADLENPFILITDKKYSNIODILPLEEVLKTNRP 243  
 QY 245 LLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGDRKKALIEDIALITGGVYITEDG 304  
 DB 244 LLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGDRKKALIEDIALITGGVYITEDG 303  
 QY 305 LEIKQATVATLGOAKITVNDKSTVVEGSSSEALNARIALISQLETTTSPDREKIQ 364  
 DB 304 LEIKQATVATLGOAKITVNDKSTVVEGSSSEALNARIALISQLETTTSPDREKIQ 363  
 QY 365 ERLAKLAGVAVIKVAPETALKEKRLIEDALNATRAVEEGIVAGGGTALITVIEKY 424  
 DB 364 ERLAKLAGVAVIKVAPETALKEKRLIEDALNATRAVEEGIVAGGGTALITVIEKY 423  
 QY 425 AALELEGDDAGRNIVYRALEEPVRIALNAGYESSVYIDLKSPAGCPNNAAGSEMD 484  
 DB 424 AALELEGDDAGRNIVYRALEEPVRIALNAGYESSVYIDLKSPAGCPNNAAGSEMD 483  
 QY 485 MIKGIIDPVKVRYSALONAAVSLITLTTAVVANKREPATPAPAMPAGDMGMMG 542  
 DB 484 MIKGIIDPVKVRYSALONAAVSLITLTTAVVANKREPATPAPAMPAGDMGMMG 541

RESULT 2  
 ID CH60\_LACLA STANDARD; PRT; 542 AA.  
 AC P37282;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).  
 GN GNL OR MORA OR GROEL OR LJO394.  
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
 CX NCBI\_TaxID=1360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93252268; PubMed=8486277;  
 RA Kim S.G., Batt C.A.;  
 RT "Cloning and sequencing of the Lactococcus lactis subsp. lactis  
 RT groEL operon".  
 RL Gene 127:121-126(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-IL1403;  
 RX MEDLINE=2135186; PubMed=11337471;  
 RA Bolotin A., Wincker P., Manger S., Jallion O., Malarme K.,  
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
 RT lactis ssp. lactis IL1403".  
 RL Genome Res. 11:751-753(2001).  
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
 CC CONDITIONS (BY SIMILARITY).  
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
 CC 7 SUBUNITS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
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 CC EMBL: X71132; CA50446.1; -  
 DR EMBL: AE006627; AAK04492.1; -  
 DR PIR: S32106; S32106.  
 DR PIR: JN0661; JN0661.  
 DR HSSP: P06139; 1GRU.  
 DR InterPro: IPR001844; Chaprnln\_Cpn60.  
 DR InterPro: IPR002423; Cpn60/TCP-1.  
 DR Pfam: PF00118; Cpn60\_TCP1.1.  
 DR PRINTS: PR00298; CHAPERONIN60.  
 DR PROSITE: PS00296; TCMPLXTCPI.  
 DR Chaperone: ATP-binding; Complete proteome.  
 RT INIT\_MET 0  
 RT SEQUENCE 542 AA; 57201 MW; D7D6P5319DA59721 CRC64;  
 SO  
 Query Match 10.3%; Score 56; DB 1; Length 542;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-41;  
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 44 GSPILTNDGVTAKETIEDHEENMGAKVSEVASKTNDIAGDGTATVTAQVY 99  
 DB 44 GSPILTNDGVTAKETIEDHEENMGAKVSEVASKTNDIAGDGTATVTAQVY 99

RESULT 3

CH60\_LACHE STANDARD; PRT: 540 AA.  
 ID CH60\_LACHE  
 AC 068324;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).  
 GN GROEL OR MOPR OR GROEL.  
 OS Lactobacillus helveticus.  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=1587;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LH212;  
 RX MEDLINE-98439363; PubMed-9766226;  
 RA Broadbent J.R., Oberg C.J., Wei L.;  
 RT "Characterization of the lactobacillus helveticus groEL operon."  
 RL Res. Microbiol. 149:247-253(1998).  
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
 CC CONDITIONS (BY SIMILARITY).  
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
 CC 7 SUBUNITS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
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 CC -----  
 DR EMBL: AF031929; AAC29004.1;  
 DR HSSP: P06139; IGRL.  
 DR InterPro: IPR001844; Chaperonin\_Cpn60.  
 DR InterPro: IPR002423; Cpn60\_TCP-1.  
 DR Pfam: PF00118; Cpn60\_TCP1.1.  
 DR PRINTS: PR00298; CHAPERONIN60.  
 DR PRINTS: PR00304; TCOMPLEXTCP1.  
 DR PROSITE: PS00296; CHAPERONIN60\_CPN60; 1.  
 KW Chaperone; ATP-binding.  
 SQ SSOURCE 540 AA; 57638 MW; 4257DB845FC7C4B4 CRC64;  
 QY 254 GEAALPTLVANKRGTFNNVAVKAPGFGDRRKA 285  
 DB 254 GEAALPTLVANKRGTFNNVAVKAPGFGDRRKA 285  
 RESULT 4  
 CH60\_LISMO STANDARD; PRT: 542 AA.  
 ID CH60\_LISMO  
 AC 09AGE6;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).  
 GN GROEL OR GROEL OR LMO2068.  
 OS Listeria monocytogenes.  
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.  
 OX NCBI\_TaxID=1639;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-L028 / Serovar 1/2c;  
 RX MEDLINE-21246697; PubMed-11349060;  
 RA Galan C.G., O'Mahony J., Hall C.;  
 RT "Characterization of the groEL operon in Listeria monocytogenes:  
 RT utilization of two reporter systems (gfp and hly) for evaluating in

RT vivo expression."  
 RL Infect. Immun. 69:3924-3932(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-EGD-e / Serovar 1/2a;  
 RX MEDLINE-21537279; PubMed-11679669;  
 RA Glaser P., Franquet L., Buchleser C., Rusnok C., Amend A.,  
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,  
 RA Charbit A., Chetoui F., Couve E., de Daruvar A., Denoux P.,  
 RA Dommann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,  
 RA Entlin K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,  
 RA Gautier L., Goebel M., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,  
 RA Madueno E., Mailounam A., Mata Vicente J., Ng E., Medjari H.,  
 RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,  
 RA Remmel B., Rose M., Schluteter T., Simoes N., Tierrez A.,  
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;  
 RT "Comparative genomics of Listeria species."  
 RL Science 294:849-852(2001).  
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
 CC CONDITIONS (BY SIMILARITY).  
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
 CC 7 SUBUNITS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
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 CC -----  
 DR EMBL: AF335323; AAK28538.1;  
 DR EMBL: AL591982; CAD00146.1;  
 DR HSSP: P06139; IGRL.  
 DR Listlist: LMO02068;  
 DR InterPro: IPR001844; Chaperonin\_Cpn60.  
 DR InterPro: IPR002423; Cpn60\_TCP-1.  
 DR Pfam: PF00118; Cpn60\_TCP1.1.  
 DR PRINTS: PR00298; CHAPERONIN60.  
 DR PRINTS: PR00304; TCOMPLEXTCP1.  
 DR PROSITE: PS00296; CHAPERONIN60\_CPN60; 1.  
 KW Chaperone; ATP-binding; Complete proteome.  
 SQ SEQUENCE 542 AA; 57367 MW; 9818B45967D92944 CRC64;  
 QY 266 RGTNNVAVKAPGFGDRRRAMEDIAIITGG 296  
 DB 266 RGTNNVAVKAPGFGDRRRAMEDIAIITGG 296  
 RESULT 5  
 CH60\_AGR5 STANDARD; PRT: 544 AA.  
 ID CH60\_AGR5  
 AC P30779;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).  
 GN GROEL OR MOPR OR GROEL OR ATU0682 OR AGR\_C1220.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93259955; PubMed-8098329;  
 RA Segal G., Ron E.Z.;



Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 273 AVKAPGDRRKAMLEIDIALITGTVI 299  
 ||||||||||||||||||||||||||||  
 DB 275 AVKAPGDRRKAMLEIDIALITGTVI 301

RESULT 7  
 CH64\_RHIME STANDARD: PRT: 545 AA.  
 ID CH64\_RHIME  
 AC 092204;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE 60 kDa chaperonin 4 (protein Cpn60 4) (groEL protein 4).  
 GN GROEL OR GROEL4 OR RA0395 OR SMA0744.  
 OS Rhizodium melioli (Rhizobium melioli).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RA MEDLINE=21396509; PubMed=11481432;  
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,  
 RA Barlow-Hubler F., Bowser L., Capela D., Gilbert F., Gouzy J.,  
 RA Gujal M., Hong A., Hultzer L., Hymen R.W., Kahn D., Kahn M.L.,  
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,  
 RA Yeh K.-C., Davis R.W., Federapoli N.A., Long S.R.;  
 RT "Nucleotide sequence and predicted functions of the entire  
 RT Sinorhizobium melioli pSyma megaplasmid.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).  
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
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 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
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 CC  
 CC -----  
 CC EMBL: AB007230; AK65053.1;  
 DR InterPro: IPR001844; Chaperin\_Cpn60.  
 DR InterPro: IPR002423; Cpn60/TCP-1.  
 DR Pfam: PF00118; Cpn60\_TCP1.1.  
 DR PRINTS: PR00304; TCOMPLEXTCP1.  
 DR PROSITE: PS00296; CHAPERONIN\_CPN60; 1.  
 KW Chaperone; ATP-binding; Heat shock; Multigene family; Plasmid;  
 KW Complete proteome.  
 SQ SEQUENCE 545 AA; 57701 MW; 498A61F23CE0431 CRC64;

Query Match 5.0%; Score 27; DB 1; Length 545;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-16;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 273 AVKAPGDRRKAMLEIDIALITGTVI 299  
 ||||||||||||||||||||||||||||  
 DB 275 AVKAPGDRRKAMLEIDIALITGTVI 301

RESULT 8  
 CH60\_BORPE STANDARD: PRT: 547 AA.  
 ID CH60\_BORPE  
 AC P48210;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).  
 GN GROEL OR MOPR OR GROEL OR Cpn60.  
 OS Bordetella pertussis.  
 OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;  
 OC Bordetella.  
 OX NCBI\_TaxID=520;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Tohama / BP338;  
 RA MEDLINE=95309719; PubMed=7789805;  
 RA Fernandez R.C., Weiss A.A.;  
 RT "Cloning and sequencing of the Bordetella pertussis cpn10/cpn60  
 RT (groSL) homolog.";  
 RL Gene 138:151-152(1995).  
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
 CC CONDITIONS (BY SIMILARITY).  
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
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 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
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 CC  
 CC -----  
 CC EMBL: U12277; AAA74967.1;  
 DR HSP: P06139; ICRL.  
 DR InterPro: IPR001844; Chaperin\_Cpn60.  
 DR InterPro: IPR002423; Cpn60/TCP-1.  
 DR Pfam: PF00118; Cpn60\_TCP1.1.  
 DR PRINTS: PR00298; CHAPERONIN60.  
 DR PRINTS: PR00304; TCOMPLEXTCP1.  
 DR PROSITE: PS00296; CHAPERONIN\_CPN60; 1.  
 KW Chaperone; ATP-binding.  
 SQ SEQUENCE 547 AA; 57481 MW; F780DD0401F63CF3P CRC64;

Query Match 5.0%; Score 27; DB 1; Length 547;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-16;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 273 AVKAPGDRRKAMLEIDIALITGTVI 299  
 ||||||||||||||||||||||||||||  
 DB 275 AVKAPGDRRKAMLEIDIALITGTVI 301

RESULT 9  
 CH60\_STANU STANDARD: PRT: 538 AA.  
 ID CH60\_STANU  
 AC 008854;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein  
 DE 60).  
 GN GROEL OR MOPR OR GROEL OR HSP60.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
 RC STRAIN=912;  
 RA MEDLINE=93290669; PubMed=7916607;  
 RA Ohta T., Honda K., Kuroda M., Saito K., Hayashi H.;  
 RT "Molecular characterization of the gene operon of heat shock proteins  
 RT HSP60 and HSP10 in methicillin-resistant Staphylococcus aureus.";  
 RL Biochem. Biophys. Res. Commun. 193:730-737(1993).  
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS

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CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC -----
CC EMBL: D14711; BAA03533.1; -
CC PIR: JN0601; JN0601.
CC HSP: P06139; 1GRL.
CC DR InterPro: IPR001844; Chaperonin_Cpn60.
CC DR InterPro: IPR002423; Cpn60/TCP-1.
CC DR Pfam: PF00118; Cpn60_TCP1.1.
CC DR PRINTS: PRO0298; CHAPERONIN60.
CC DR PRINTS: PRO0304; TCOMPLEXTCP1.
CC DR PROSITE: PS00296; CHAPERONINS_CPN60/ 1.
CC KW Chaperone; ATP-binding; Heat shock.
CC FT INIT_MET 0
CC SQ SEQUENCE 538 AA; 57722 MW; 58173E21A6EAC15E CRC64;

Query Match 4.88; Score 26; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 3,9e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 SDFREKLEQLERLAKLAVVAVIKYA 381
Db 356 SDFREKLEQLERLAKLAVVAVIKYA 381

RESULT 10
CH60_LISTIN STANDARD; PRT; 542 AA.
AC 0928V0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN GROEL OR GROEL OR LIN2174.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacilliales; Listeriaceae; Listeria.
CC NCBI_TaxID=1042;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN-CLIP 11262 / Serovar 6a;
CC RX MEDLINE-21537279; PubMed-11679669;
CC RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
CC Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
CC Charablt A., Cherouani F., Couve E., de Daruvar A., Deboux P.,
CC Domnan E., Dominguez-Bernal G., Duchaud E., Durant L., Dusurget O.,
CC Entian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
CC Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
CC Jones L.-M., Kaerst U., Krell J., Kuhn M., Kunst F., Kurapkat G.,
CC Madeno E., Maltoniun A., Mata Vicente J., Ng E., Nedjari H.,
CC Nordstlek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
CC Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
CC Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
CC "Comparative genomics of Listeria species.";
CC Science 294:849-852(2001).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC -----

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CC -----
CC EMBL: AL596171; CAC97403.1; -
CC DR listlist: LIN02174; -
CC DR InterPro: IPR001844; Chaperonin_Cpn60.
CC DR InterPro: IPR002423; Cpn60/TCP-1.
CC DR Pfam: PF00118; Cpn60_TCP1.1.
CC DR PROSITE: PS00296; CHAPERONINS_CPN60/ 1.
CC KW Chaperone; ATP-binding; Complete proteome.
CC SQ SEQUENCE 542 AA; 57301 MW; 68B6AD2A730DB709 CRC64;

Query Match 4.88; Score 26; DB 1; Length 542;
Best Local Similarity 100.0%; Pred. No. 3,9e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 266 RGFNVVAVKAPGFGRRKAMLEDA 291
Db 266 RGFNVVAVKAPGFGRRKAMLEDA 291

RESULT 11
CH65_RHIME STANDARD; PRT; 542 AA.
AC P35471;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 60 kDa chaperonin 5 (protein Cpn60 5) (groEL protein 5).
GN GROEL5 OR GROEL5 OR GROEL-C OR RB1006 OR SBE21566.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid psymb (megaplasmid 2).
CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC Rhizobiaceae; Sinorhizobium.
CC NCBI_TaxID=382;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN-1021;
CC RX MEDLINE-93231539; PubMed-8097179;
CC RA Rusinganwa E., Gupta R.S.,
CC "Cloning and characterization of multiple groEL chaperonin-encoding
CC genes in Rhizobium meliloti.";
CC RT gene 126:67-75(1993).
CC RN [12]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN-1021;
CC RX MEDLINE-21396508; PubMed-11481431;
CC RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
CC Vorholter F.J., Hernandez-Lucas I., Becker A., Couzy J.,
CC Golding B., Puelher A.;
CC "The complete sequence of the 1,683-kb psymb megaplasmid from the N2-
CC fixing endosymbiont Sinorhizobium meliloti.";
CC Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC -----
DR EMBL: M94191; AAA26287.1;
DR EMBL: AL603645; CAC94906.1;
DR PIR: JN0512; JN0512.
DR HSSP: P06139; IGRU.
DR InterPro: IPR001844; Chaprin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PRO0298; CHAPERONIN60.
DR PRINTS: PRO0304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW Chaperone; ATP-binding; Heat shock; Multigene family; Plasmid;
FT Complete proteome.
FT CONFLICT 239 A -> R (IN REF. 1).
FT CONFLICT 400 L -> V (IN REF. 1).
FT CONFLICT 504 A -> G (IN REF. 1).
FT CONFLICT 534 LPRAG -> FRPR (IN REF. 1).
SQ SEQUENCE 542 AA; 57882 MW; 200FAC54B6736245 CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 1; Length 542;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 273 AVKAPGCDRRKAMLEDAITLGTG 298
DB 275 AVKAPGCDRRKAMLEDAITLGTG 300

RESULT 12
CH60_BACST STANDARD; PRT; 539 AA.
AC 007201;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN GROEL OR MOXA OR GROEL.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Geobacillus.
OX NCBI_TaxID=1422;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NUB36;
RX MEDLINE=93224474; PubMed=8096641;
RA Schoen U., Schumann W.,
RT "Molecular cloning, sequencing, and transcriptional analysis of the
RT groEL operon from Bacillus stearothermophilus.";
RL J. Bacteriol. 173:2465-2469(1993).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC -----
DR EMBL: I10132; AAA22752.1;
DR HSSP: P06139; IGRU.
DR InterPro: IPR001844; Chaprin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PRO0298; CHAPERONIN60.
DR PRINTS: PRO0304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW Chaperone; ATP-binding; Heat shock.
KM

OY 272 VAVKAPGCDRRKAMLEDAITLGTG 296
DB 272 VAVKAPGCDRRKAMLEDAITLGTG 296

RESULT 13
CH60_CLOTM STANDARD; PRT; 540 AA.
AC P48212;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (HSP-60).
GN GROEL OR MOXA OR GROEL.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NCIB 10682;
RX MEDLINE=97199381; PubMed=9047357;
RA Ciruela A., Cross S., Freedman R.B., Hazlewood G.P.;
RT "Sequence and transcriptional analysis of groEL and groEL genes from
RT the thermophilic bacterium Clostridium thermocellum.";
RL Gene 186:143-147(1997).
RN (2)
RP SEQUENCE OF 1-20.
RC STRAIN=NCIB 10682;
RX MEDLINE=96257758; PubMed=8687408;
RA Cross S.J., Ciruela A., Pocomutca K., Romaniec M.P.M., Freedman R.B.;
RT "Thermostable chaperonin from Clostridium thermocellum.";
RL Biochem. J. 316:615-622(1996).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC -----
DR EMBL: Z68137; CAA92242.1;
DR HSSP: P06139; IGRU.
DR InterPro: IPR001844; Chaprin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PRO0298; CHAPERONIN60.
DR PRINTS: PRO0304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW Chaperone; ATP-binding.
FT INIT MET 0
FT CONFLICT 14 15 LE -> ML (IN REF. 2).
FT CONFLICT 20 20 Q -> K (IN REF. 2).
SQ SEQUENCE 540 AA; 57343 MW; A638C71A2675C396 CRC64;

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 540;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 272 VAVKAPGCDRRKAMLEDAITLGTG 296

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Db 271 VAVKAPGEGDRKAMLEIDIALITGG 295

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RESULT 14
CH60_BACHD STANDARD: PRT: 544 AA.
AC 050305: 09KFC3:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN GROEL OR MOPR OR GROEL OR BH0562.
OS Bacillus halodurans.
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RA MEDLINE=97141316; PubMed=9987660;
RA Xu Y., Kobayashi T., Kudo T.;
RT "Molecular cloning and nucleotide sequence of the groEL gene from the
RT alkaliphilic Bacillus sp. strain C-125 and reactivation of thermally
RT inactivated alpha-glucosidase by recombinant GROEL."
RL Biosci. Biotechnol. Biochem. 60:1633-1636(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RA MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirata C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC EMBL: D55630; BAA09494.1;
DR EMBL: AP001508; BAB04281.1;
DR HSSP: P06139; 1GRL.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; cpn60_TCP1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PROSITE: PS00296; CHAPERONINS_CPN60.1.
KM Chaperone; ATP-binding; Heat shock; Complete proteome.
FT CONFLICT 407 421 E -> VR (IN REF. 1).
FT CONFLICT 421 421 MISSING (IN REF. 1).
FT CONFLICT 500 500 A -> VP (IN REF. 1).
FT CONFLICT 512 512 MISSING (IN REF. 1).
SQ SEQUENCE 544 AA: 57403 MW: 6769ED81C903C971 CRC64;
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Query Match 4.6%; Score 25; DB 1; Length 544;  
Best Local Similarity 100.0%; Pred. No. 3e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
272 VAVKAPGEGDRKAMLEIDIALITGG 296  
|||||

Db 272 VAVKAPGEGDRKAMLEIDIALITGG 296

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|||||
RESULT 15
CH60_BURCE STANDARD: PRT: 546 AA.
AC 092FED:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN GROEL OR MOPR OR GROEL.
OS Burkholderia cepacia (Pseudomonas cepacia).
OC Bacteria: Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxID=292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 10744;
RA Zysk G., Spletstoesser W.D., Neubauer H.;
RT "Nucleotide sequence comparison of the groE operon of Burkholderia
RT spp."
RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
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CC EMBL: AF104907; AAC79087.1;
DR HSSP: P06139; 1GRL.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; cpn60_TCP1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PROSITE: PS00296; CHAPERONINS_CPN60.1.
KM Chaperone; ATP-binding.
SQ SEQUENCE 546 AA: 56980 MW: 174B9934345E7315 CRC64;
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Query Match 4.6%; Score 25; DB 1; Length 546;  
Best Local Similarity 100.0%; Pred. No. 3e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
272 VAVKAPGEGDRKAMLEIDIALITGG 296  
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Job time : 28 secs